

ProMOL User Guide

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Introduction

ProMOL was created as a plug-in to the molecular visualization program PyMOL, found at <http://www.pymol.org/>. The plug-in ProMOL was implemented in Python and can be accessed from the plug-in menu in PyMOL versions 0.99, 1.0, 1.1, 1.2, and 1.4 after extraction to the appropriate directory. It is supported for Windows XP, Windows 7, Linux, and Mac. ProMOL also works with PyMOL version 1.3 in Windows XP, Windows 7 and Mac OS X; there are some problems with the Python library in Linux that interfere with ProMOL function in PyMOL 1.3 for Linux. The source code for the ProMOL plug-in and a PyMOL build containing the ProMOL plug-in are freely available for download from <http://sourceforge.net/projects/sbevsl/files/ProMOL/>.

Installation

Windows, Macintosh, Linux and Unix

The ProMOL plug-in is available as a compressed file of a folder which contains the plug-in file (ProMOL.py) and a folder (ProMOL) which contains files used by ProMOL. The compressed file is available for download in both .zip and .tar.gz formats.

- 1) Install PyMOL. ProMOL is a plugin for PyMOL. PyMOL is available as an open source program from

<http://sourceforge.net/projects/pymol/>

and is incorporated into many Unix and Linux releases. PyMOL is also available in proprietary versions from

<http://www.pymol.org>.

See that website for information on PyMOL licensing. PyMOL is a program that was written by the late Warren DeLano. PyMOL is a trademark of Schrodinger, LLC. ProMOL is a plugin for PyMOL, not a derivative part of PyMOL, but depends on having a copy of PyMOL in order to operate. Therefore, in order to use ProMOL, you first must have a copy of PyMOL installed.

Download PyMOL from <http://pymol.sourceforge.net> and install to the default location on your system.

For installation of PyMOL on an MS Windows system (ProMOL has been tested with PyMOL 0.99, 1.0, 1.1, 1.3 and 1.4), see

http://pymolwiki.org/index.php/Windows_Install

For installation of PyMOL on a Mac under OS X (ProMOL has been tested with PyMOL 0.99, 1.0, 1.1, 1.3 and 1.4), see

http://pymolwiki.org/index.php/MAC_Install

For installation of PyMOL on a Linux system (ProMOL has been tested with PyMOL 0.99, 1.0, 1.1, 1.2 and 1.4) see

http://pymolwiki.org/index.php/Linux_Install

- 2) Download ProMOL. ProMOL can be downloaded in a compressed file format from

<http://sourceforge.net/projects/sbevsl/files/>

in the ProMOL folder. It is important to note that clicking on the prominent green download arrow on this page (or the main SBEVSL page on SourceForge.net) may lead you to another file that is part of the SBEVSL project. You will need to open the ProMOL folder on <http://sourceforge.net/projects/sbevsl/files> by clicking on the green triangle to the left of the ProMOL folder. Similarly, you should download the latest ProMOL version, which will be the compressed file at the top of the file list..

You can choose to download either the .zip or .tar.gz compressed file, depending on your preferences and your operating system.

Unix or Linux

- 1) Expand the compressed file. In unix or linux systems, or using MINGW under Windows you may unpack the tarball with

```
gunzip < ProMol-4.2.tar.gz | tar xvf -
```

- 2) Install ProMOL. Plugins that consist of a single python file (e.g. plugin.py) can be installed simply by using the Plugin->Manage Plugins->Install... menu. However, this does not work with ProMOL because you need to install the ProMOL folder as well as the promol.py file. So you will need to take the following steps:

- a) Find the startup folder in your PyMOL installation. For the default installation of PyMOL 1.2 under Ubuntu linux, you can find the startup folder in /usr/lib/pymodules/python2.7/pmg_tk/startup.
- b) Simply place the ProMol.py and ProMOL folders inside the startup folder. The next time you launch PyMOL, ProMOL should appear in your Plug-ins menu.
- c) If you have installed PyMOL to another location on your system, you will need to copy ProMol.py and the ProMOL folder to the location of the pymol installation tree that contains

modules/pmg_tk/startup

Once you have completed the installation, launch PyMOL and look for ProMOL in the Plugin menu. When all files are in place, the ProMOL gui can be opened by selecting ProMOL from the plugin menu.

Windows

- 1) Expand the compressed file. Windows systems may have a native application that will expand your .tar.gz or .zip files; if not you may wish to consider using Stuffit Expander or WinZip.
- 2) Install ProMOL. Plugins that consist of a single python file (e.g. plugin.py) can be installed simply by using the Plugin->Manage Plugins->Install... menu. However, this does not work with ProMOL because you need to install the ProMOL folder as well as the promol.py file. So you will need to take the following steps:
 - a) Find the startup folder in PyMOL. In the default Windows installation of PyMOL 1.3, you can find the startup folder at

c:\Program Files\PyMOL\PyMOL\modules\pmg_tk\startup

- b) Install ProMOL by copying ProMol.py and the ProMOL folder to the startup folder. If you have installed PyMOL to another location on your system, you will need to find the portion of the PyMOL installation tree that contains

modules\pmg_tk\startup

Once you have completed the installation, launch PyMOL and look for ProMOL in the Plugin menu. When all files are in place, the ProMOL gui can be opened by selecting ProMOL from the plugin menu.

Macintosh

- 1) Rename your MacPyMOL application (for MacPyMOL ONLY, not pymol). Under Mac OS X, if you have MacPyMOL (as opposed to pymol installed using fink or macports) you will need use a copy of the MacPyMOL application (MacPyMOL.app) renamed PyMOLX11Hybrid (PyMOLX11Hybrid.app), in order to get access to plugins. This is not

necessary for the versions of pymol (as opposed to MacPyMOL) installed using fink or macports.

- 2) Expand the compressed file. Macintosh systems may have a native application that will expand your .tar.gz or .zip files; if not you may wish to consider using Stuffit Expander.
- 3) Plugins that consist of a single python file (e.g. plugin.py) can be installed simply by using the Plugin->Manage Plugins->Install... menu. However, this does not work with ProMOL because you need to install the ProMOL folder as well as the ProMol.py file. This can be a bit tricky on the Mac, so follow these instructions closely if you have MacPyMol renamed as PyMOLX11Hybrid:
 - a) Find the startup folder in PyMOL.
 - i) Open Finder -> Applications
 - ii) If you have a three button mouse, right click on MacPyMOLX11Hybrid and select Show Package Contents. This will take you to the directory tree for PyMOL. If you don't have a three button mouse, Ctrl-click should bring up the option to Show Package Contents.
 - iii) Traverse the tree to pymol/modules/pmg_tk/startup.
 - b) Copy ProMol.py and the ProMOL folder to the startup folder.

If you installed PyMOL to some other location (e.g. using fink or macports), you will need to find the portion of the pymol installation tree that contains

modules/pmg_tk/startup

and place promol.py and the ProMOL folder in the startup folder. For example in a fink PyMOL installation for python 2.4, 2.5 or 2.6 under Macintosh OSX, the promol.py file and the ProMOL folder belong under

/sw/lib/pymol-py24/modules/pmg_tk/startup or
 /sw/lib/pymol-py25/modules/pmg_tk/startup or
 /sw/lib/pymol-py26/modules/pmg_tk/startup

Note: Any version of python below 2.6 may not be compatible with the latest ProMOL release.

- 4) Once you have completed the installation, launch PyMOL and look for ProMOL in the Plugin menu. When all files are in place, the ProMOL gui can be opened by selecting ProMOL from the plugin menu.

Special Notes for Installing ProMOL Under Mac OS X

There are several alternate versions of PyMOL for use under Mac OS X. In order to install ProMOL, you need to use a version of PyMOL that accepts plugins. In the example above, a "fink" installation was assumed. Alternatively you may wish to use a MacPorts install, or to install MacPyMOL. You will find instructions for all three at

http://pymolwiki.org/index.php/MAC_Install

However, it is important to note that in order to have access to plugins and be able to install ProMOL, you need to use an X11 version, rather than an Aqua version. MacPyMOL works both ways. In order to tell MacPyMOL to work with X11 and make plugins available, you need to rename MacPYMOL.app to

PyMOLX11Hybrid.app first.

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Components

The ProMOL interface has 5 tabs (Welcome, EZ-Viz, Motif Finder, Motif Maker, and View Options) as well as 6 buttons at the base of the GUI (Open, Fetch PDB, Random PDB, Clear, and Help) that are always available. The following pages describe the use of the Buttons and Tabs.

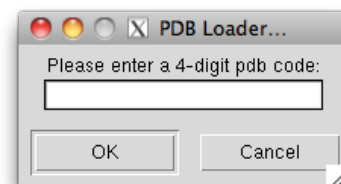
Buttons on the ProMOL GUI

The buttons on the bottom of the screen appear whenever ProMOL is open.

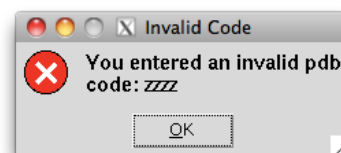


Open PDB opens a dialog box that will let you search any storage devices connected to your computer for PDB files.

Fetch PDB opens a dialog box that allows you to open a PDB file over the Internet, using the PDB Loader Service, a plug-in that is available on all PyMOL builds. If you enter an invalid PDB code, you receive an error message, "You have entered an invalid pdb code: " followed by the code you entered. The sample image was generated by entering "zzzz" as the PDB code.



Random PDB loads a PDB file selected at random. This is a handy tool if you wish to test for true negatives and false positives when designing and testing motifs (see the sections about the Motif Maker and Motif Finder tabs).



Clear removes all structures that are visible in the molecular viewing screen.

Help is currently being re-implemented and does not function at this time.

Welcome. The *Welcome* tab is also the opening screen for ProMOL that identifies the plugin.

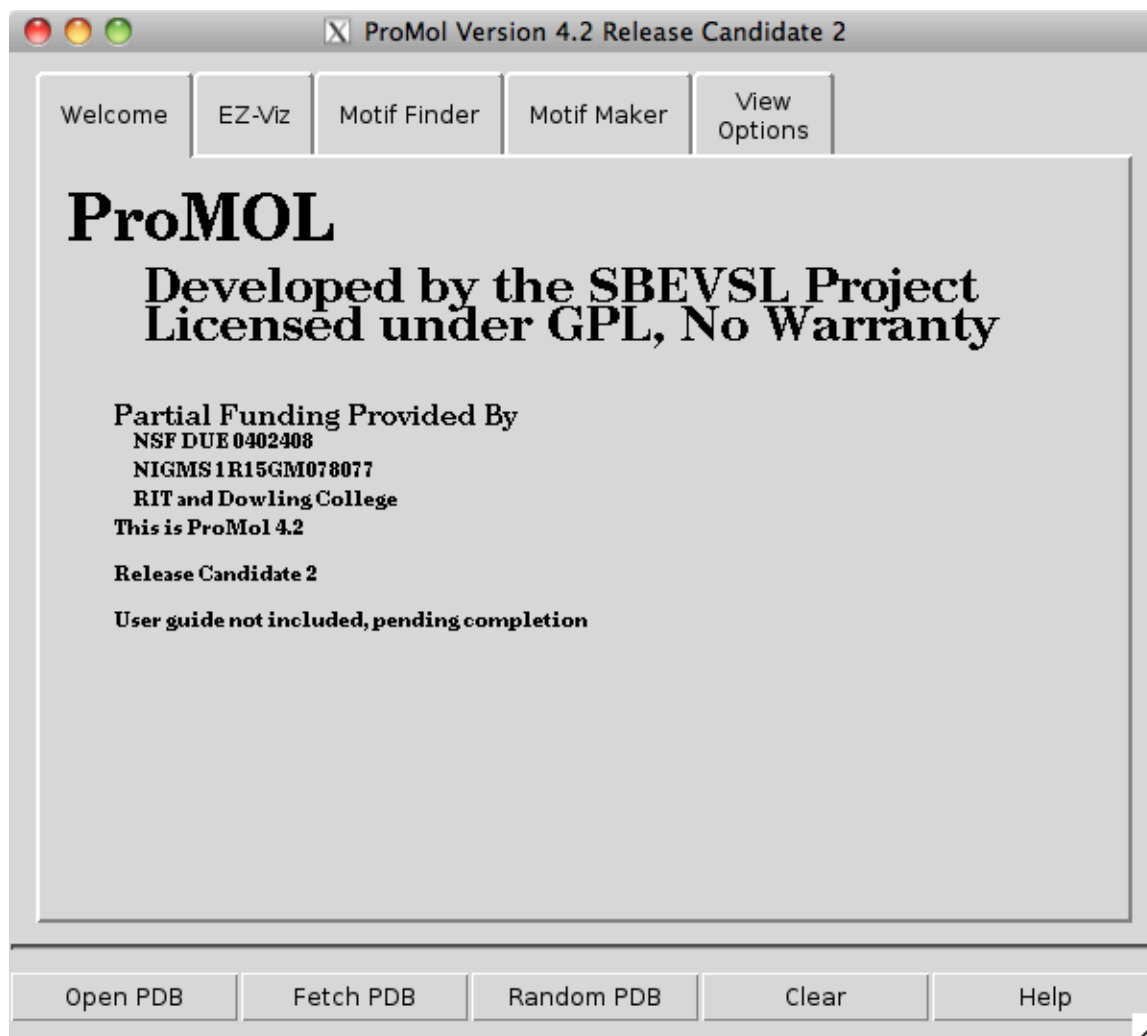


Figure 1. The ProMOL welcome screen. ProMOL is released under a Gnu Public License (<http://www.gnu.org/licenses/gpl.html>). The screen credits refer to funding from the National Institutes of General Medical Sciences, a division of the National Institutes of Health, and to the National Science Foundation Division for Undergraduate Education.

EZ-Viz. The *EZ-Viz* tab includes most of the functionality from the EZ-Viz plugin as described in the paper by Grell et al. [Grell, L., Parkin, C., Slate, L., Craig, P.A. EZ-Viz, a Tool for Simplifying Molecular Viewing in PyMOL. *Biochemistry and Molecular Biology Education*, **34**, 402-407 (2006)]. Earlier versions of EZ-Viz and ProMOL contained a very simplified PyMOL to Chime/Rasmol/Jmol command convertor. This converter has been updated and enhanced dramatically with the ConScript plug-in for PyMOL [Mottarella, S.E., Rosa, M., Bangura, A., Bernstein, H.J., Craig, P.A. ConSCRIPT: *Biochemistry and Molecular Biology Education*, **38**, 419-421 (2010)]. The ConScript plug-in and user manual can be obtained from <http://sourceforge.net/projects/sbevsl/>.

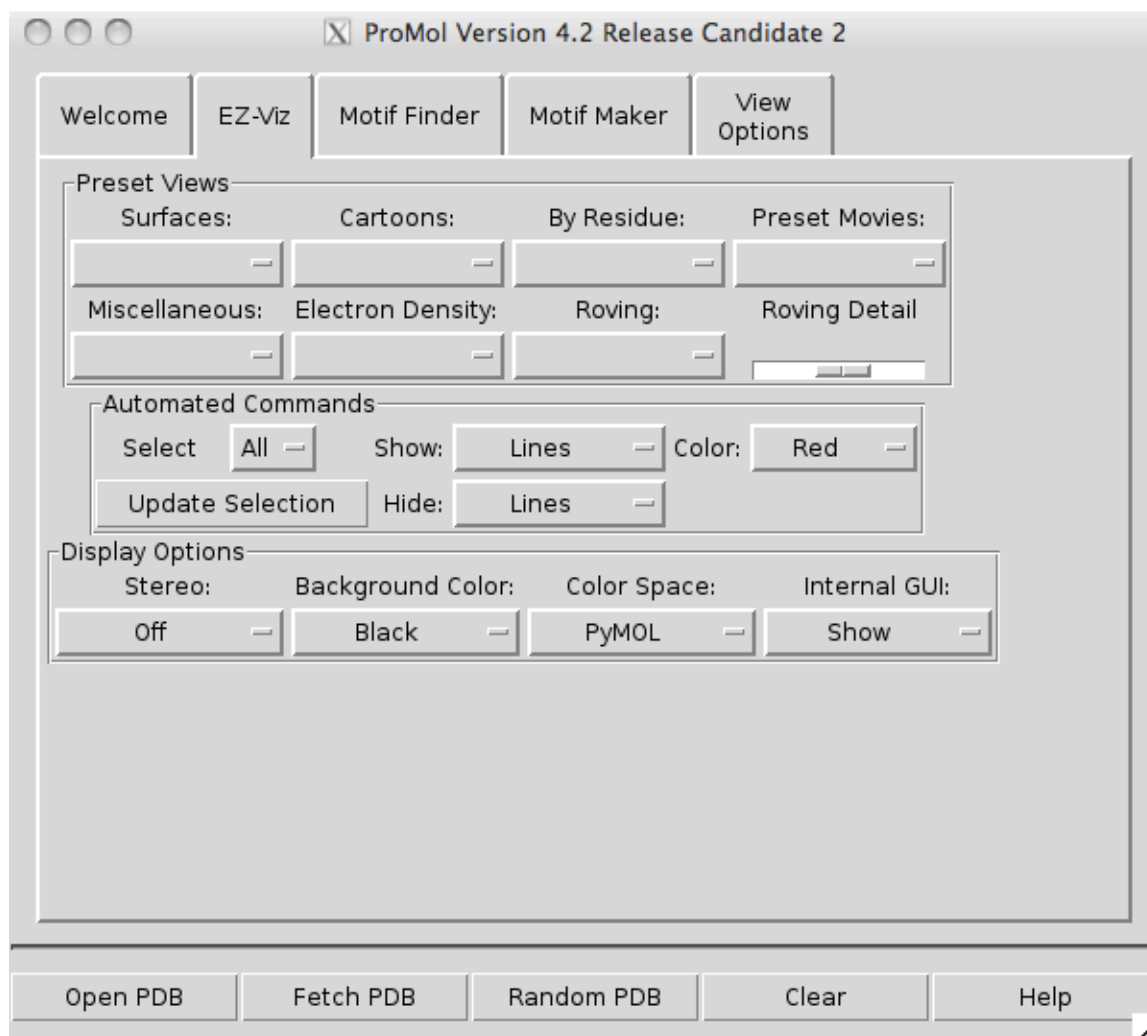
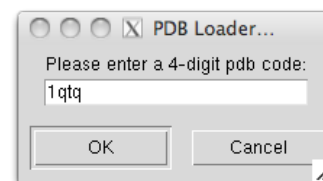


Figure 2. The EZ-Viz tab in ProMOL enables users to create interesting views and movies of their macromolecular structures using the drop down menus, once a protein is loaded. Users can then manipulate their structures without having to learn and use Python commands.

Using EZ-Viz. Let's begin by opening a PDB file in PyMOL. You can do this using the Fetch PDB button on the bottom of the ProMOL GUI. You will need to enter the PDB ID for a structure of interest in the popup window that appears and click on the OK button. For this manual, we will use 1qtq (glutaminyl tRNA synthetase complexed with tRNA and an amino acid analog).



When you do this, the structure will appear in the PyMOL viewer window as a simple stick figure, where each stick represents a bond between two atoms in the structure (Figure 3).

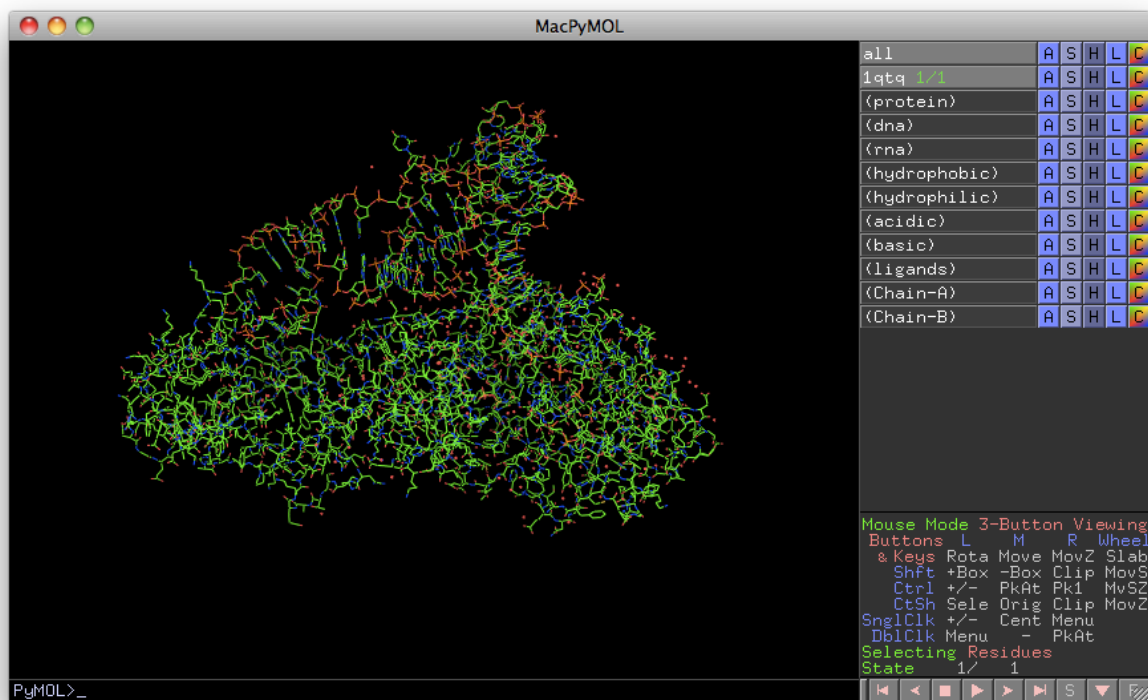


Figure 3. The appearance of 1qtq on loading in PyMOL.

You can change the appearance of this structure to generate a number of different views using the options in the *Preset Views* area on the EZ-Viz tab. For example, if you select Cartoons from the Cartoon menu, you then generate this view, which shows the protein as a cartoon, the DNA as a stick structure and the waters as spheres (Figure 4). You can remove the waters from the image simply by selecting Water from the Hide menu in the *Automated Commands* area of EZ-Viz (Figure 5). The select, show, color and hide commands in this area are designed to enable users to manipulate the appearance of the structure without having to enter scripts. *Display Options* support changing the status of the stereo mode, background color, color palette and the internal GUI for PyMOL, which appears on the right hand side of the viewer window. The internal GUI contains a list of selections within PyMOL, information about the Mouse Mode in PyMOL and the control buttons for movies within PyMOL.

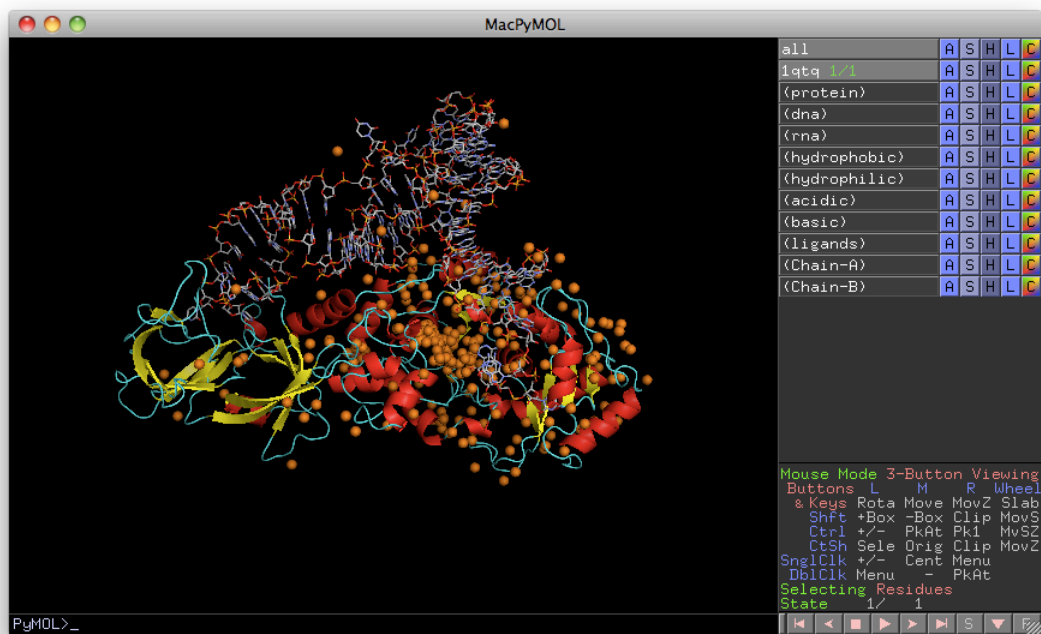


Figure 4. The Cartoon version of 1qtq as implemented in EZ-Viz.

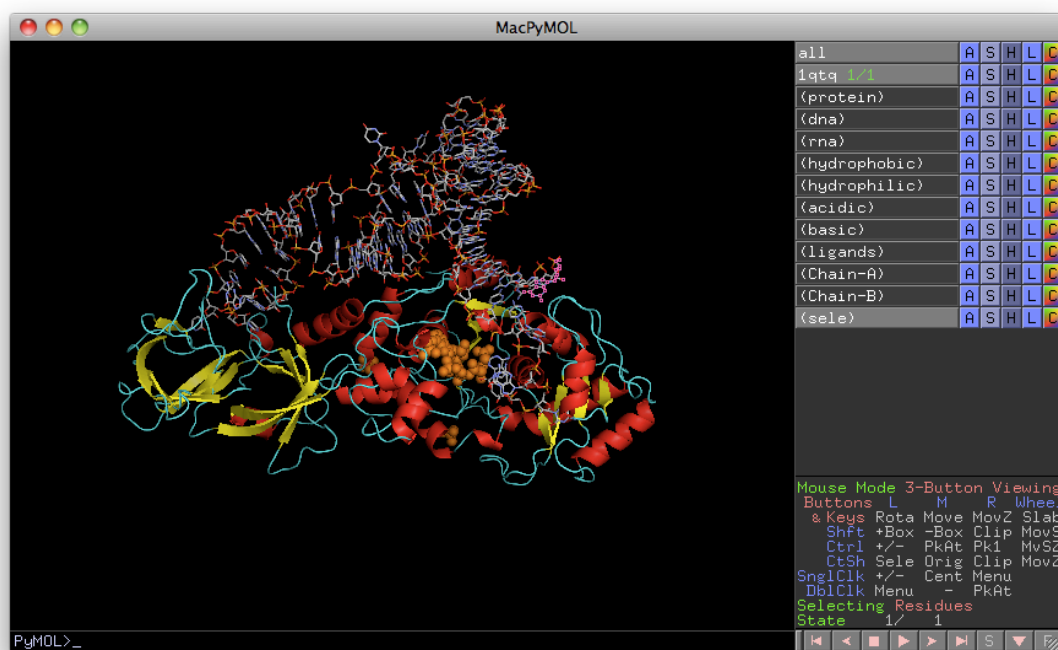


Figure 5. The Cartoon version of 1qtq as implemented in EZ-Viz after hiding the waters.

Motif Finder. The *Motif Finder* tab gives the user access to the motif search tools in ProMOL (Figure 6). The ProMOL code contains four sets of motifs based on three different approaches to catalytic site alignment:

1. The JESS C_αC_β motifs are based on two atoms for each of the residues known to participate in a catalytic site, based on the listings in the Catalytic Site Atlas (<http://www.ebi.ac.uk/thornton-srv/databases/CSA/>). The JESS template files can be obtained from <http://www.ebi.ac.uk/thornton-srv/databases/cgi-bin/CSS/makeEbiHtml.cgi?file=downloadTemplateLibrary.html>.
2. The JESS functional atom motifs are based on the two atoms (C_α and C_β) as well as a third atom found in the side chain.
3. The ProMOL motifs were built using the ProMOL Motif Maker (found in the Motif Maker tab), utilizing the same catalytic residues identified in the CSA. The distances between each atom from each of the residues in a catalytic site were measured using PyMOL's built in measurement function. These measured distances were used to create the three-dimensional motif definition for that catalytic site.
4. The UserMotifs are the ones that have been created by the user with ProMOL. On the Mac, they can be found in the folder, /Users/***username***/Library/Application Support/SBEVSL/ProMol/UserMotifs.. Windows: %AppData%/SBEVSL/ProMol/. Unix: ~/.sbevsl/ProMol

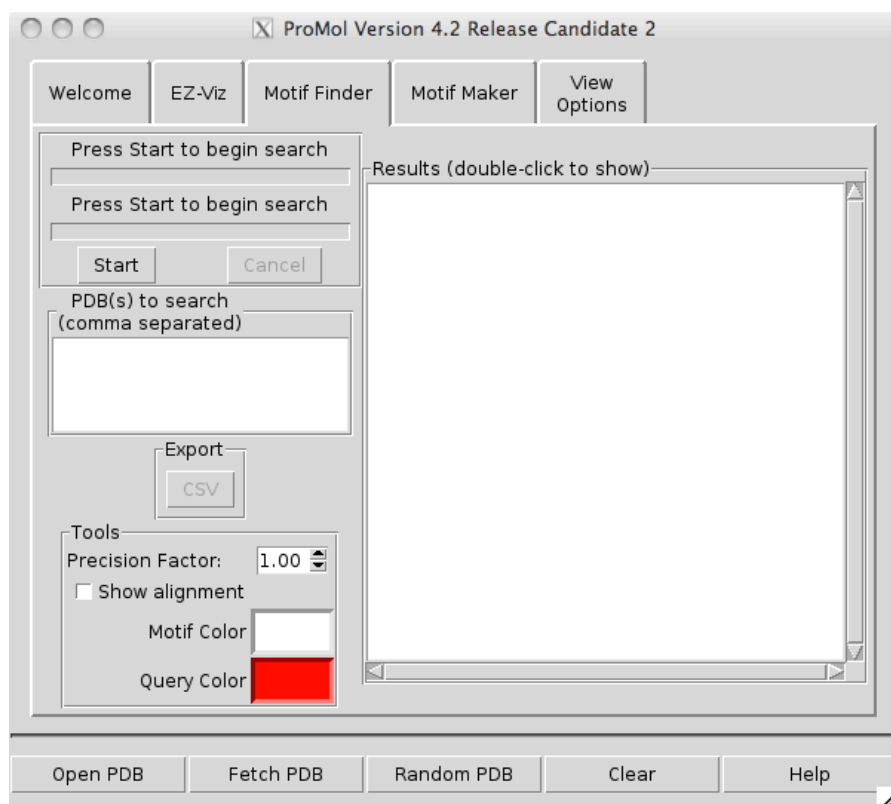


Figure 6. The Motif Finder tab in ProMOL.

To use the Motif Finder, a protein must be loaded into PyMOL. You can do this by entering a PDB id in the box labeled “PDBs to search”. If you would like to search more than one structure at a time, just enter the PDB ids separated by commas.

Once the PDB IDs have been entered, click the Start button to begin searching for motifs. A popup window (Figure 8) allows the user to choose which set of motifs he would like to search against. For this manual, a search of all motifs was performed, but this takes a while (about 5 – 8 minutes per query structure against 200 motifs). If you are focused only on 5 motifs you have created yourself, the search is much quicker. Once you have chosen your motif set, the search begins. On the search window (Figure 7), the top bar indicates the search progress on the individual structure currently under evaluation and the bottom bar indicates overall progress for the full list of structures that are under evaluation.

Warning: Do not click on the results of the Motif Finder while it is still running, as this will produce incorrect results. Also, do not load, clear, or modify any structures or selections while the Motif Finder is running, for the same reason.

When the search is complete, the results will appear in the box on the right side of the Motif Finder tab. The results are reported by PDB ID in a scrollable window (Figure 9). In the Motif Maker output window, the format for each template is Score_motif-group_pdb-template-fileid_EC#.

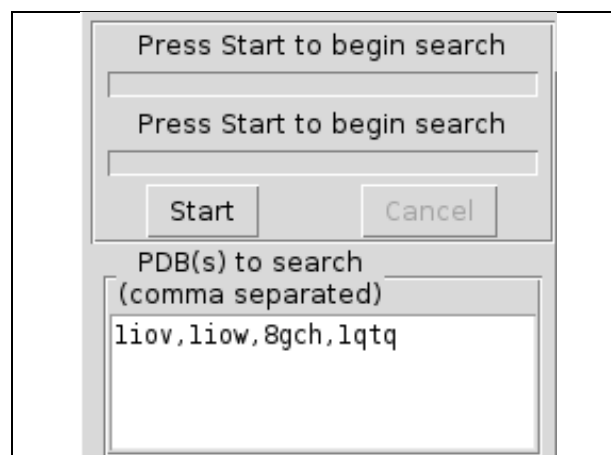


Figure 7. Entering the PDB IDs to search

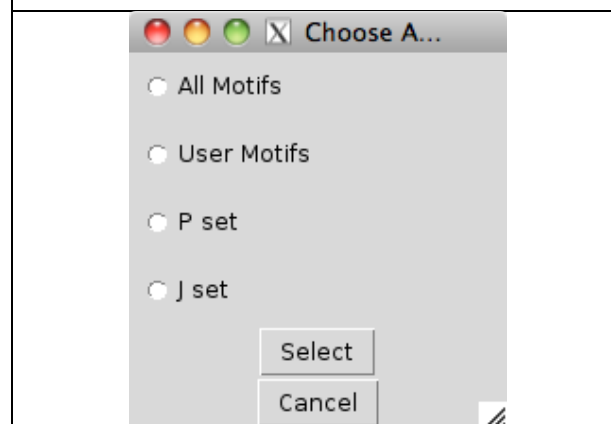


Figure 8. Choosing the motif sets to search.

- **Score.** The results are assigned a value ranging from 0 to 4. Each alignment is given a score based on a Levenshtein distance, which reflects the number of differences between the query structure (1qtq in Figure 9) and the template motifs that are listed there. In simple terms, the Levenshtein distance from the word “horse” to the word “house” is 1, since you need to change the 3rd letter from an “r” in horse to a “u” in house. In the example shown, two structures report a Levenshtein distance of 0, meaning that there are no changes – all of the amino acids in the active site of the template structure have been found in the active site of the query structure. The second result is a comparison of 1qtq to itself, so a Levenshtein distance of 0 is expected. There is also a Levenshtein distance of 0 from 1djg to 1qtq. This is a bit of a surprise, considering that 1qtq is a glutaminyl tRNA synthetase while 1djg is a trimethylamine dehydrogenase.
- **Motif-group.** There are currently five motif groups in ProMOL:
 - Jab means the motif is a member of the JESS C_αC_β group.
 - Jfa means the motif is a member of the JESS functional atom group.
 - Pab means the motif is a member of the ProMOL group that was designed with the PDB template used for the comparable Jab motif.
 - Pfa means the motif is a member of the ProMOL group that was designed with the PDB template used for the comparable Jfa motif. A designation of P means only that the Pab and Pfa motifs were identical as created by ProMOL.
 - U means that this is a motif the user created using Motif Maker.
- **Template-file** is the PDB ID for the structure that was used to build the template.
- **EC#** is the Enzyme Commission number as reported by the Protein Data Bank.

We can compare the active sites for 1djg and 1qtq directly using the alignment tools found on the lower left hand corner of the Motif Finder tab. Simply click the Show alignment check box (Figure 10), then double click on the template motif that you want to

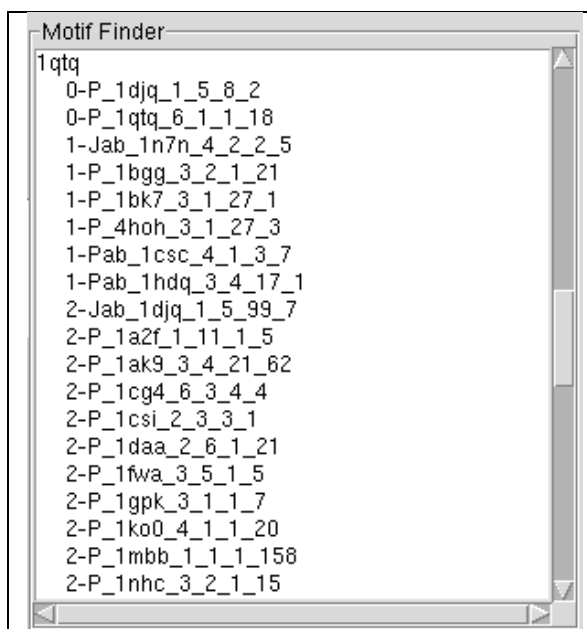


Figure 9. Motif Finder Search Results for 1qtq.

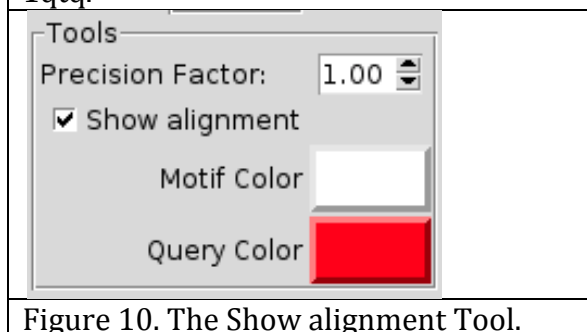


Figure 10. The Show alignment Tool.

superimpose on the query motif (P_1djg-1_5_8_2 in this case). The result is shown in Figure 11. The alignment is not perfect, but the three residues (aspartate 267, histidine 172 and tyrosine 169 in 1djg; aspartate 219, histidine 215 and tyrosine 211 in 1qtg) are found in similar proximity in the two structures. Note: The result that bears the full name of the template motif (P_1djg_1_5_8_2 in the image below) can be ignored. Use the two “match_in” selections (match_in_1qtg and match_in_1djg in the image below) to manipulate the alignment.

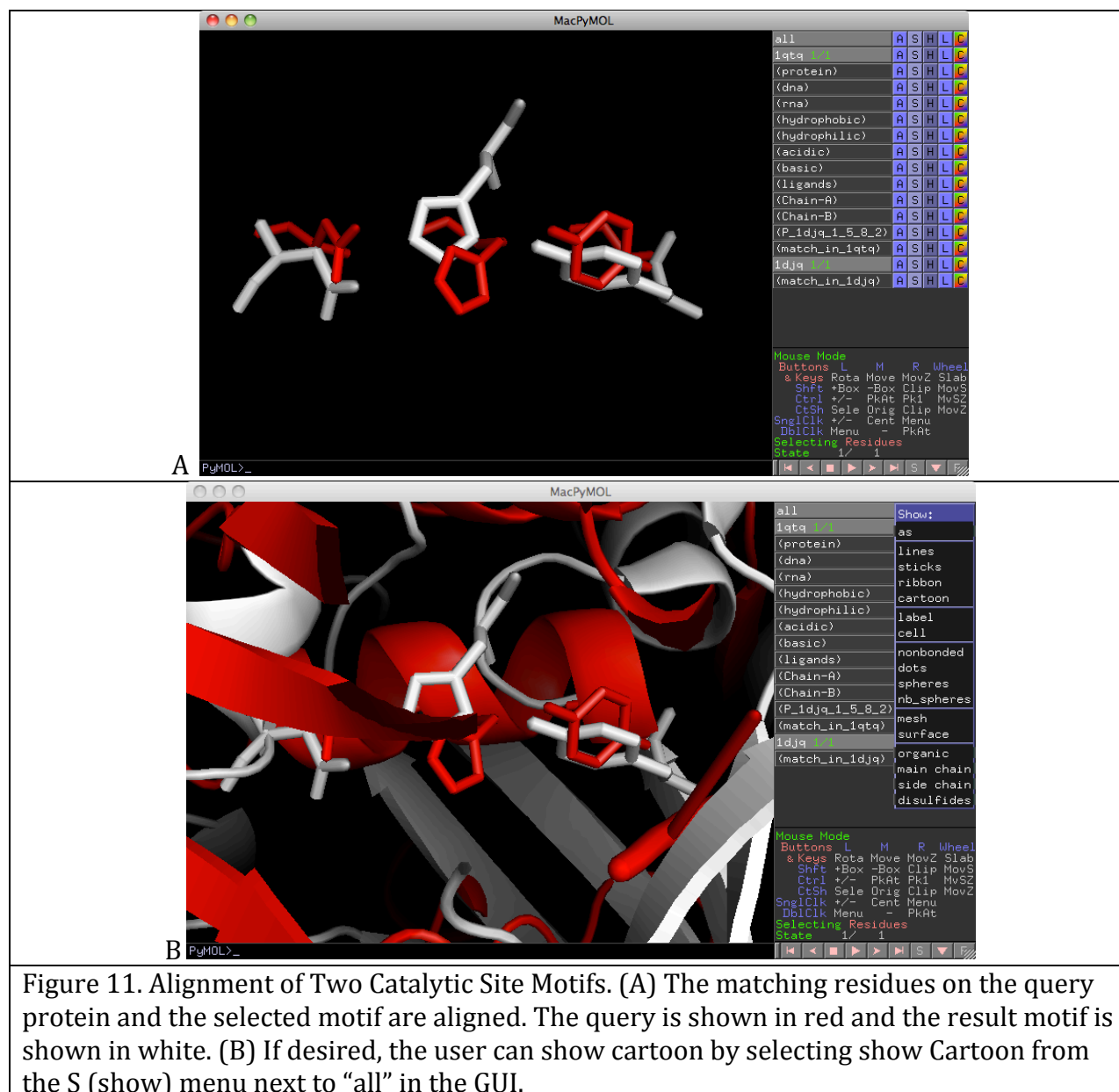
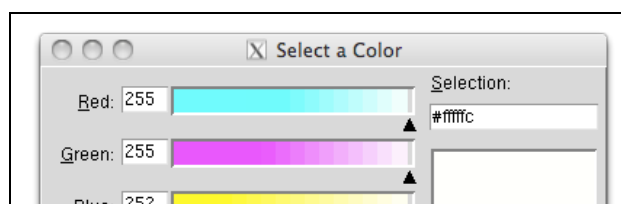


Figure 11. Alignment of Two Catalytic Site Motifs. (A) The matching residues on the query protein and the selected motif are aligned. The query is shown in red and the result motif is shown in white. (B) If desired, the user can show cartoon by selecting show Cartoon from the S (show) menu next to “all” in the GUI.



It is possible to change the colors used in the alignment by clicking on the colored square next to either Template Color or Motif Color in the Show

Alignment toolbox on the Motif Finder tab. You can also click on individual residues in the PyMOL viewer window and the residue will be identified in the PyMOL GUI. For 1qtq, you will receive this notice if you click on the beta carbon from Glutamate residue=34, "You clicked /1qtq//A/GLU'34/CB".

Figure 12. Color Selection Dialog Box for Structural Alignments.

Motif Maker

The *Motif Maker* tab (Figure 14) enables the user to build motifs based on definitions in the Catalytic Site Atlas. Motif definitions in ProMOL are based on enzyme family representatives selected from the PDB and information from the CSA. The distances between each atom from each of the residues in a catalytic site were measured using PyMOL's built in measurement function (Figure 13). These measured distances were used to create the three-dimensional motif definition for that catalytic site. The motif definitions are then used to predict the presence of a catalytic site on the structure being tested.

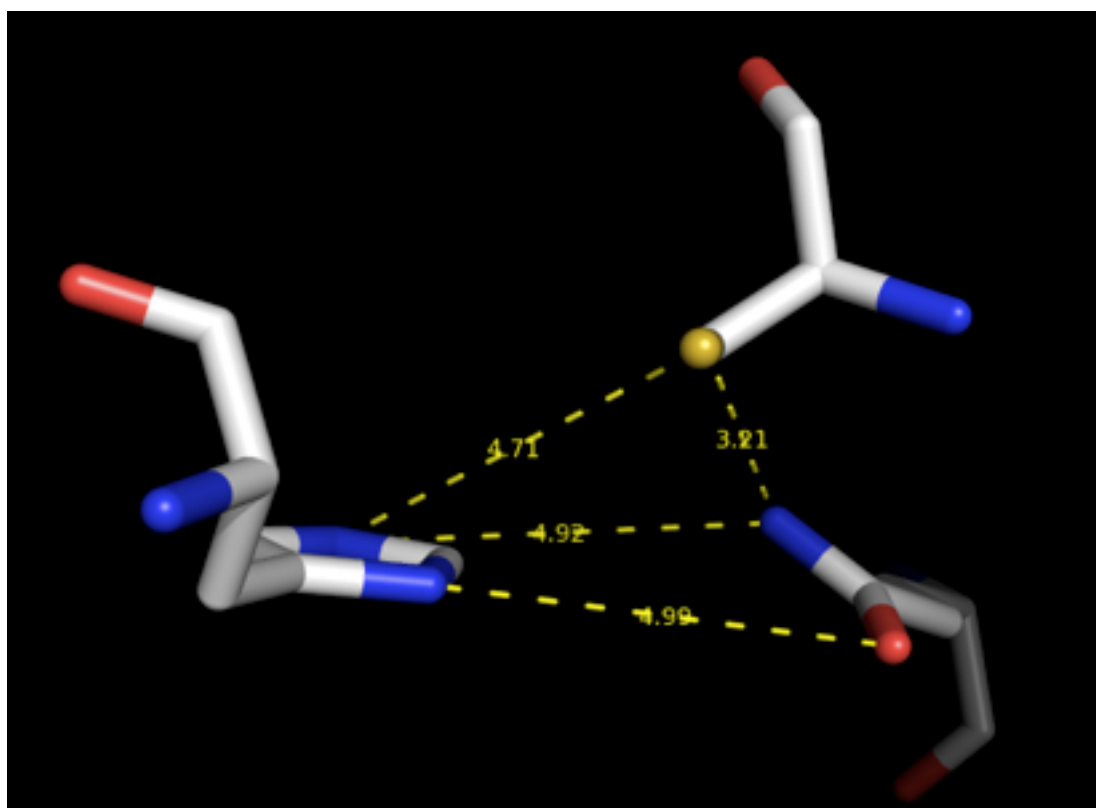


Figure 13. Measurements between atoms in active site residues in a serine protease. The distances between various atoms on each residue displayed by PyMOL are used to create the three-dimensional active site motif definition. Calculations are based on the PDB entry 1AB9, gamma chymotrypsin.

Here is a step-by-step description of how to create a motif for 3 α -hydroxysteroid dehydrogenase type 3, based on pdb entry 1j96.

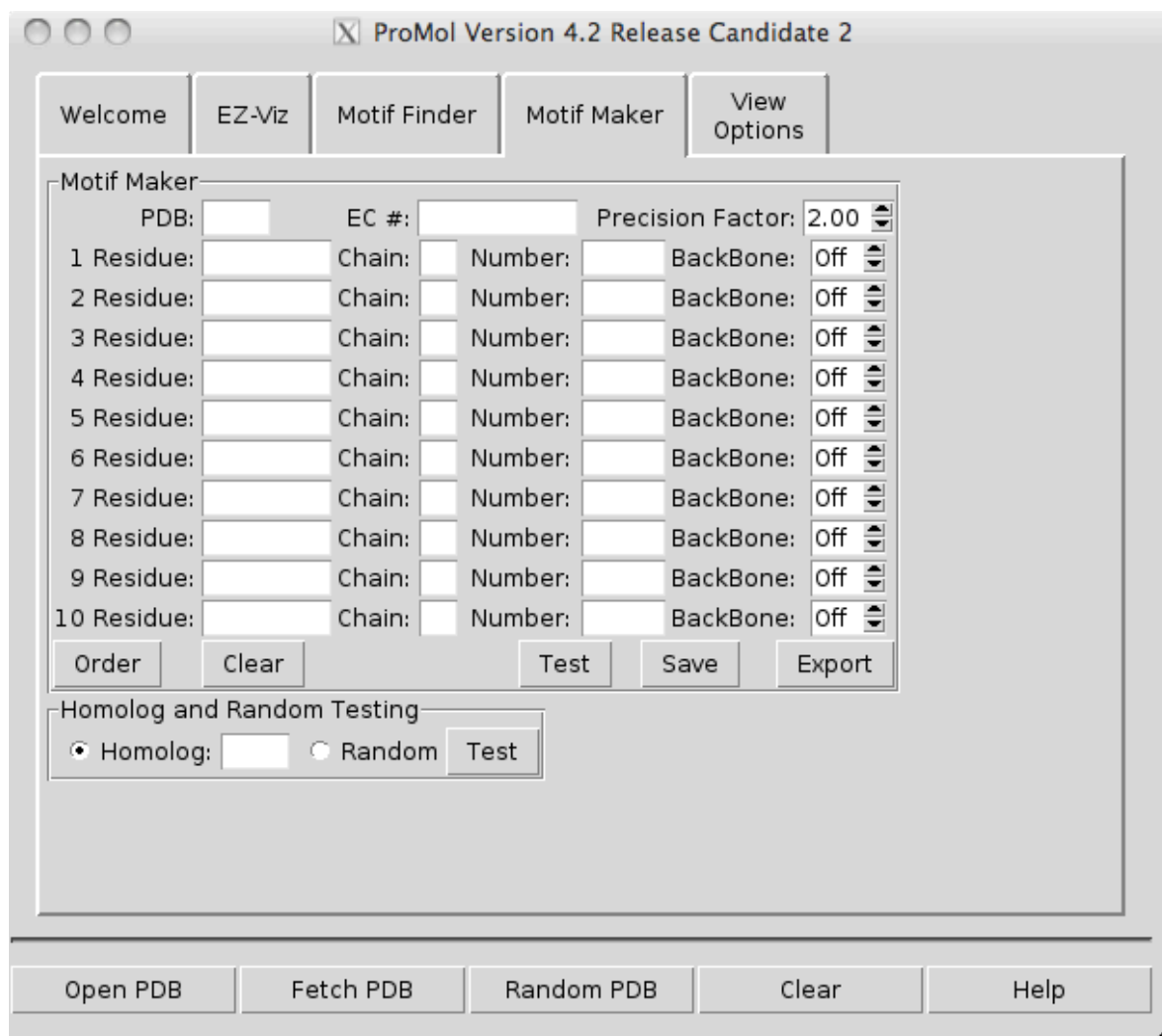


Figure 14. The Motif Maker tab.

3 α -hydroxysteroid dehydrogenase type 3 (PDB id 1j96) is an annotated entry in the Catalytic Site Atlas (CSA; http://www.ebi.ac.uk/thornton-srv/databases/cgi-bin/CSA/CSA_Site_Wrapper.pl). Simply open the CSA in a browser, enter 1j96 (or the desired structure) in the PDB code box and hit the Search button. The page shown in Figure 15 should appear.

CSA entry for 1j96 Homologous Entry

Title:	Oxidoreductase		
Compound:	3alpha-hydroxysteroid dehydrogenase type 3		
Mutant:	No		
UniProt/Swiss-Prot:	P52895-DBDI_HUMAN	EC Class:	1.3.1.20
Other CSA Entries:	Homologues of 1j96 Entries for UniProt/Swiss-Prot: P52895 Entries for EC: 1.3.1.20		Other Databases: PDB entry: 1j96 PDBsum entry: 1j96 UniProt/Swiss-Prot: P52895 IntEnz entry: 1.3.1.20

Sites:

☒ Catalytic Site (Get help with this section)

Found by: PsiBLAST alignment on 1mrq (Structural analysis and templates exist for the 1mrq family)

Residue	Chain	Number	UniProt number	Functional part
ASP	A	50	50	Sidechain
TYR	A	55	55	Sidechain
LYS	A	84	84	Sidechain
HIS	A	117	117	Sidechain

Figure 15. The Catalytic Site Atlas page for 1j96.

To build a motif, you'll need several pieces of information about a structure that you can find on the CSA page: its PDB ID, its EC#, and the residues that constitute its active site (Figure 14). This information for 3 α -hydroxysteroid dehydrogenase type 3 was entered into the Motif Maker window as shown in Figure 16.

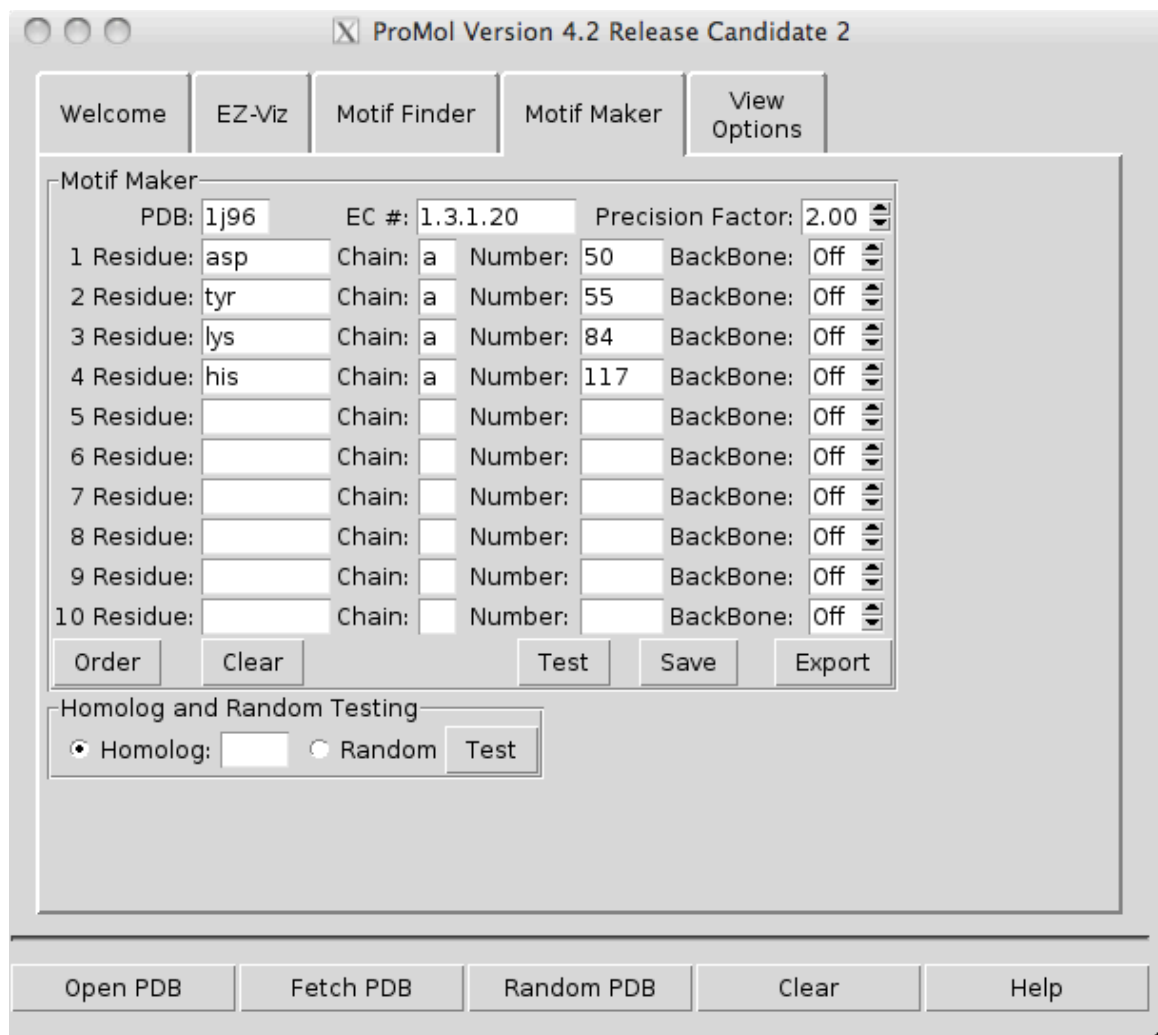


Figure 16. The Motif Maker window with entry locations for four residues in 3 α -hydroxysteroid dehydrogenase type 3 (PDB id 1j96).

Once a motif has been entered in Motif Maker, it can be tested on the template structure by clicking the test button found in the Motif Maker box. A test of this motif yielded an immediate match of only the desired residues. If additional residues appear (often due to the distance between residues in some catalytic sites), there are ways to adjust the motif to select the desired residues. First, the precision factor can be reduced. The precision factor is a multiplier that is applied to the distances between the residues in the catalytic site. The next adjustment is made by turning the backbone atoms on – this simply adds the backbone atoms for the residues into the motif definition. The motif definition can sometimes be improved by changing the order of the residues as they are entered in the Motif Maker box; it is often advantageous to list the residues in the order of least common in a structure to most common in that same structure.

Once you are satisfied with a motif, click on the Save button in the Motif Maker box and the motif will be saved to your computer; the exact location depends on your operating system.

- Macintosh: The motif definition file is saved as U_1j96_1_3_1_20.py to
/Users/<user name>/Library/Application Support/SBEVSL/ProMol/UserMotifs/
- Windows 2000/XP: The motif definition file is saved as U_1j96_1_3_1_20.py to
C:\Documents and Settings\<user name>\Application Data\SBEVSL\ProMol\UserMotifs\
- Windows 7: The motif definition file is saved as U_1j96_1_3_1_20.py to
C:\Users\<user name>\AppData\Roaming\SBEVSL\ProMol\UserMotifs\
- Linux: The motif definition file is saved as U_1j96_1_3_1_20.py to
~/.sbevsl/ProMol/UserMotifs/

The next step in designing a motif is to test it against homologs. A list of homologs can be found on the Catalytic Site Atlas by clicking the Homologues of 1j96 link (or the selected structure) found under Other CSA Entries. In the case of 1j96, more than 100 homologs are listed. To test a homolog, first enter the PDB code in the Homolog and Random Testing box on the Motif Maker window, then click the test button in the same box. Table 1 contains a list of structures tested and briefly summarizes the results. The first 10 homologs listed in the CSA were tested, then homologs found 10, 20 and 40 positions later in the table were tested.

Homolog #	PDB id	Active Site Found?	Extraneous or Missing Residues
	1j96	Yes. Asp50, Tyr55, Lys84, His117	None
1	1mrq	Yes. Asp50, Tyr55, Lys84, His117	None
2	2alr	Yes. Asp44, Tyr49, Lys79, His112	Asp170
3	2acu	No	No Tyrosine in the active site
4	1a80	No It was found if the Precision Factor was increased to 2.3.	Asp45, Tyr50, Lys75, His108
5	1abn	No	No motif found. The PDB file is alpha carbons only and won't work with ProMOL
6	1ads	Yes. Asp43, Tyr48, Lys77, His110	No
7	1ae4	No	No. Alpha carbons only
8	1afs	Yes. Asp50, Tyr55, Lys84, His117 in both Chains A and B	No
9	1ah0	Yes. Asp43, Tyr48, Lys77, His110	No
10	1ah3	Yes. Asp43, Tyr48, Lys77, His110	No
20	1el3	Yes. Asp 43, Tyr48, Lys77, His110	No

30	1lwi	Yes. Asp50, Tyr55, Lys84, His117 in both chains A and B	No
50	1s2a	Yes. Asp50, Tyr55, Lys84, His117	

Table 1. Homolog testing for the 1j96 motif, 3 α -hydroxysteroid dehydrogenase type 3.

When a new motif is built in Motif Maker, it should be tested with 10 or more homologs of the structure. The purpose of this testing is to look for **true positives** – structures in which ProMOL clearly identifies the existing motif correctly. Some may match perfectly; others may match poorly or not at all. In the case of a poor or non-existent match, the researcher then needs to explore the structure. Typical reasons for a poor match are substitutions in the structure (perhaps a serine was replaced with a lysine by site-directed mutagenesis to give a more stable crystal), the absence of the catalytic site (homology is based on the entire sequence, not just the few residues in the catalytic site), or an overly constrained motif maker definition file.

The next stage in motif testing is a search for **false negatives** – structures that ProMOL incorrectly identifies as containing the motif. To that end, we usually test the motif against 10 randomly selected PDB files. This is done by clicking the Random radio button in the Homolog and Random Testing box, then clicking on the test button 10 times. The 1j96 motif was tested 10 times on randomly selected files (1dzk, 2l35, 1e4d, 2mgc, 1pic, 1u6j, 2eq7, 1ztz, 1q8o, 1krc) and none returned an active site. For this limited test then, no false positives were returned.

View Options

Users can visit the View Options tab (Figure 17) to adjust the way PyMOL generates images of their structures. The Preset Views box of the EZ-Viz tab enables users to generate interesting views of structures without coding in Python. The View Options tab can then be used to adjust the appearance of cartoons, spheres, sticks, and surfaces found in a structure; it is also possible to adjust the ambient light, much as a photographer would adjust the lighting in an indoor studio to provide the best view.

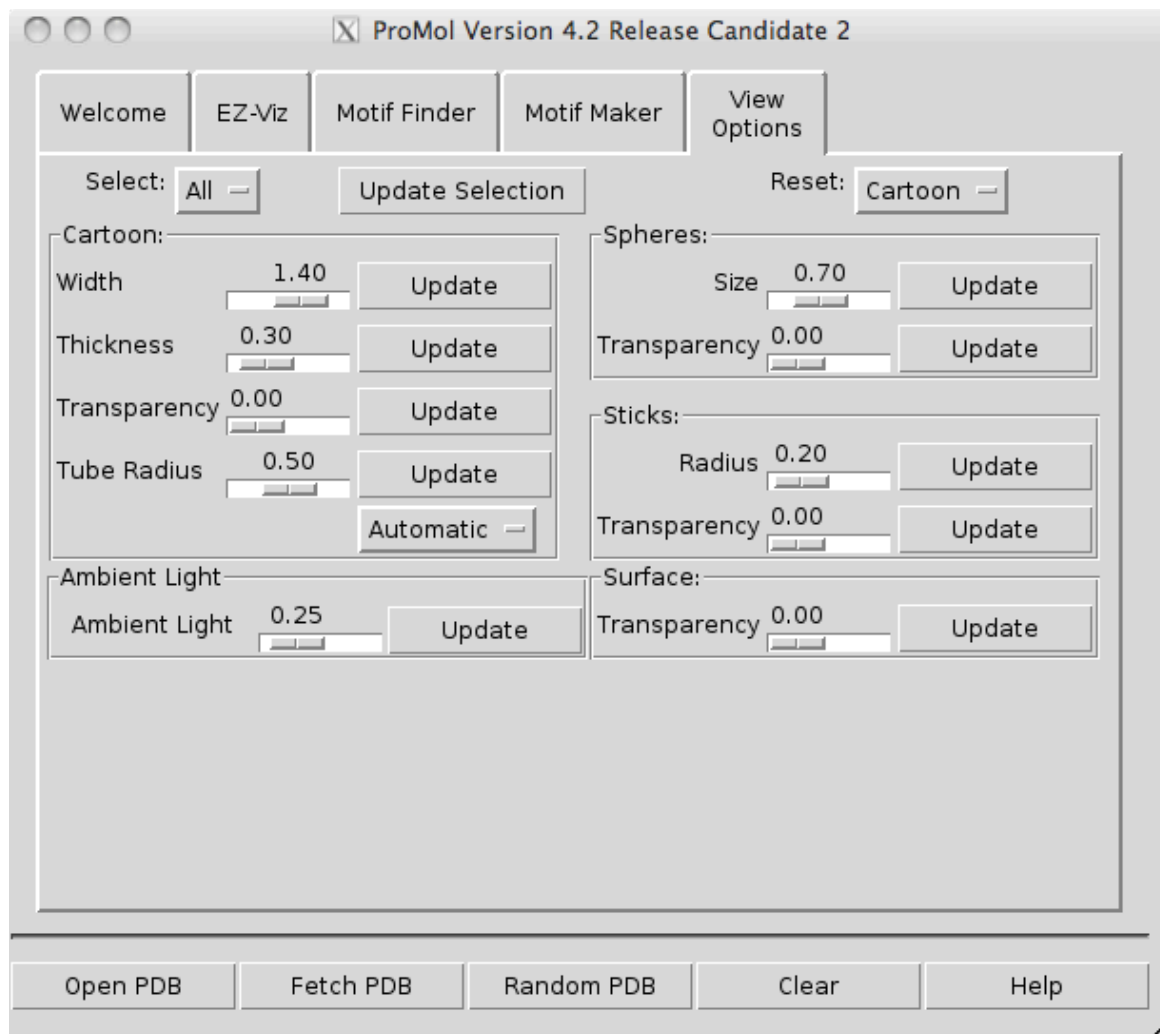


Figure 17. The View Options Tab in ProMOL can be used to adjust the default settings for cartoon, sphere, stick and surface values, in addition to adjusting the ambient lighting.

One of two examples will be provided here; users are encouraged to play with the options to see if the cartoon view can be made more interesting by, for example, changing the tube radius in the Cartoon box on the View Options tab. Figure 18 shows the default cartoon generated from the EZ-Viz tab for GAL4, a transcriptional factor from yeast that is bound to a 17 residue DNA sequence, followed by some adjustments from the default values.

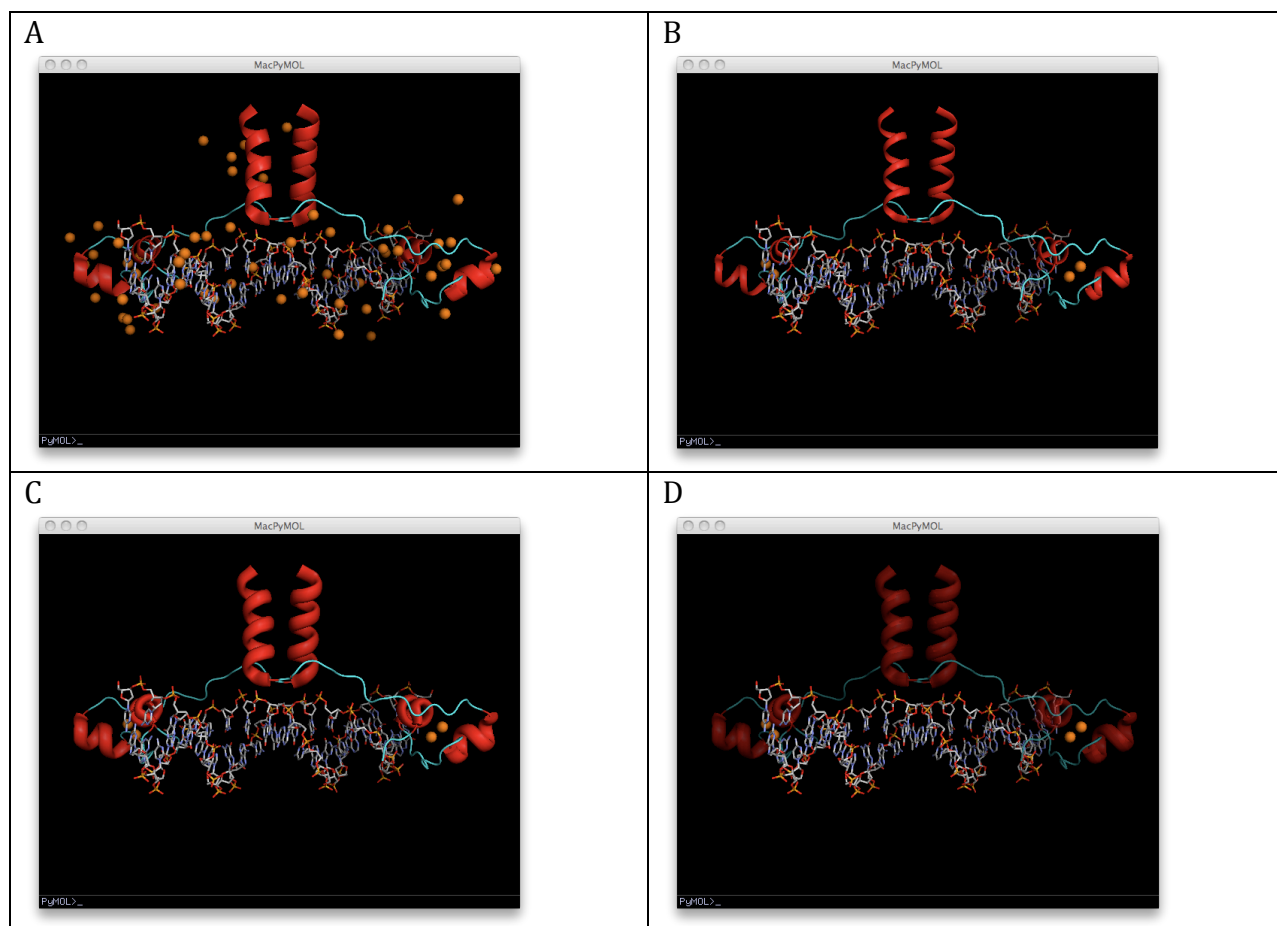


Figure 18. (A) The first image shows the default EZ-Viz cartoon for a DNA-protein complex (PDB is 1d66). (B) The waters have been hidden (EZ-Viz Hide Water) and on the View Options tab, Cartoon Width has been reduced from 1.40 to 0.75. (C) the Cartoon Width has been returned to 1.40, while the Cartoon Thickness has been increased from 0.30 to 0.80. (D) The transparency for the protein part of the 1d66 has been changed from 0.0 to 0.50, without affecting the appearance of the DNA.

Users are encouraged to experiment with the View Options for use in demonstrations in class and also for use in publications.